Indian J. Genet., 70(1): 22-28 (2010)

Combining ability and stability studies for grain yield and quality parameters in QPM (*Zea mays* L.) inbred line crosses

P. Shanthi[1] , G. Suresh Babu , E. Satyanarayana[2] and R. Sai Kumar[2]

Department of Genetics and Plant Breeding, Allahabad Agriculture Institute, Deemed University, Allahabad 211 007

(Received: May 2009; Revised: December 2009; Accepted: January 2010)

Abstract

Studies on combining ability, stability and G x E interaction were carried out at two locations (Hyderabad and Allahabad) and in two seasons (*Kharif* 2003 and *Kharif* 2004) for grain yield and three quality parameters *viz.,* protein content, oil content and tryptophan content in 45 single cross hybrids developed using 10 x 10 diallel set (excluding reciprocals). From this study it is inferred that, the three hybrids P_4 x P_7, P_2 x P_6 and P_5 x P_{10} were considered as most stable and good specific combiners for grain yield and quality parameters (protein, oil and tryptophan content) along with higher *per se* values for the four characters studied. These hybrids can be exploited as better QPM hybrids for commercialization across the wide environments through heterosis breeding and also for the derivation of QPM inbred lines in segregating generations. Among the ten parents, the parents P_3 and P_1were found to be the best parents for grain yield, while, the parents P_4, P_7 and P_2 for protein, oil and tryptophan content.

Key words: QPM, *Zea mays* L., stability, combining ability, grain yield, quality parameters

Introduction

Maize is the second most important cereal crop in the world. Although maize is mainly considered as a source of carbohydrate but it is also an important source of protein because of its considerable total protein yield per hectare [1]. The protein content of maize seed has nutritional value and it was demonstrated that increase of protein percent could be possible by breeding [2]. Quality protein maize (QPM) is the nutritionally rich maize since two essential amino acids tryptophan and lysine are present in higher quantities than in normal maize. Apart from these two characters with global acceptance of maize oil, it can be considered as a rich source of nutritive oil with least detrimental effect on human health. Hence, attention has also been diverted to high oil maize [3].

The knowledge of gene action and combining ability helps in identifying the best combiners which may be hybridized either to exploit heterosis or to accumulate genes through selection and in understanding the characters to choose the proper selection method to be followed in breeding programmes.

A desirable hybrid should possess stability in performance besides high yield. The high yielding ability and response to environmental changes are the two independent attributes of a genotype and are governed by separate gene system [4, 5]. A stable phenotypic expression of a character is the result of interaction between its genotype and the environment in which it develops. In view of this, present investigation was undertaken to study the stability and combining ability effects, by evaluating the 45 QPM single cross hybrids, developed using 10 x 10 diallel set over four environments for grain yield and three quality parameters *viz.,* protein content, oil content and tryptophan content.

Materials and methods

The experimental material for the present investigation comprised of ten promising elite quality protein maize genotypes (*viz.*, P_1, P_3, P_5, P_7, and P_9 lines are of dent grain type and the remaining five lines P_2, P_4, P_6, P_8 and P_{10} are of flint grain type), 45 F_1 cross combinations along with two standard checks (DHM 105-Normal maize hybrid (Better yielding check) and Shaktiman 2 – QPM hybrid) at two locations (Hyderabad and Allahabad) and in two season (*Kharif* 2003 and *Kharif*

Present address: [1]Winter Nursery Center, D.M.R., Rajendranagar, Hyderabad 500 030
[2]Deptt. of Genetics & Plant Breeding, ANGRAU, Rajendranagar, Hyderabad

2004). The 45 F_1 single cross hybrids were developed by crossing ten QPM parental inbred lines in diallel mating design as suggested by Griffing [6] excluding reciprocals during *rabi* 2002-2003 at ARS, Amberpet, Hyderabad, A.P, with an objective of identifying lines with high *gca* and crosses with high *sca* and to study the combining ability and gene action. The experimental material was grown in complete randomized block design with three replications. Each genotype was planted in a single row of 5m length with a row to row and plant to plant spacing of 75 cm and 20 cm respectively. Grain yield per plot (Kg) and three important quality characters *viz.,* protein content (%), oil content (%) and tryptophan content (g/16g N) were recorded on five randomly selected plants in each plot excluding border plants in each replication for all the genotypes in all the four environments. Data were analyzed as per Griffing in method II and model I to estimate combining ability effects and followed the model proposed by Eberthart and Russell [7] to estimate the three parameters of stability namely mean, regression coefficient (bi) and mean squared deviation (S^2 di) for each genotype.

Results and discussion

(i) Combining ability studies

In the present investigation, the combining ability analysis revealed significant mean squares due to general and specific combining ability effects indicating that both additive and non-additive gene actions involved in the inheritance of grain yield, protein content, oil content and tryptophan content. The analysis of GCA and SCA variances showed that four characters studied were controlled preponderantly by non-additive gene action since, specific combining ability variance (SCA) was greater than general combining ability variance (GCA) (Table 1). These results are in concurrence with investigations carried out by earlier researchers [1, 8-10]. Under these circumstances, for exploiting non-additive gene action and to improve these characters one has to resort to the breeding procedures, which lead to heterozygous end products such as recurrent selection and reciprocal recurrent selection.

Among the ten parents studied, considering the two locations and two seasons, the parental lines P_3 and P_1 can be given the status of good general combiners and genetically worthy parents, followed by P_{10} as they expressed highest significant values of GCA effects and contributing maximum favourable genes for grain yield. Where as, three parents *viz.,* P_4, P_2 and P_7 are found to be good general combiners with significant *gca* effects along with higher *per se* values for protein, oil and tryptophan content and consistent over locations and seasons (Tables 2 & 3). Hence, these three parents can be better utilized for the simultaneous improvement of protein, oil and tryptophan content. Where as P_6 was also good combiner for protein and oil content over four environments and for tryptophan content over three environments. In the same way, parent P_9 showed significant *gca* effects for only tryptophan content over three environments. Hence, these two parents (P_6 and P_9) having desired quality parameters can be used in improving the characters and also as a donor parents for these characters in addition to P_4, P_2 and P_7 parents. Similar type studies were previously carried out [9, 11-14].

Out of 45 single crosses studied, 27 crosses exhibited significant *sca* effect at all the locations and seasons for grain yield. But, based on *sca* effects, the best specific combination found out for high grain yield is P_4 x P_7 followed by P_3 x P_9, P_2 x P_6, P_5 x P_{10}, P_1 x P_8, P_3 x P_8, P_3 x P_6, P_1 x P_5, P_3 x P_5, P_1 x P_{10} and P_3 x P_{10} (Table 2 & Table 4), which were also showed higher grain yield on *per se* (*i.e.,* more than 4.00 kg grain yield per plot) and it should be noticed that, these eleven

Table 1. Analysis of variance for combining ability for grain yield and quality parameters pooled over four environments

Source	d.f.	Protein content (%)	Oil content (%)	Tryptophan content (g/16g N)	Grain yield per plot (kg)
GCA	9	1.19825**	0.55800**	0.01905**	1.20930**
SCA	45	0.46350**	0.31367**	0.00488**	0.97980**
Error	108	0.08375	0.04400	0.00069	0.00085
σ^2 gca		0.00700	0.00375	0.00007	0.00008
σ^2 sca		0.07950	0.04175	0.00079	0.00089
σ^2 gca / σ^2 sca		0.08825	0.09050	0.09075	0.08875

Table 2. Details and *per se* performance of ten parental lines used in diallel programme and *per se* performance of eleven best hybrids pooled over four environments

Entry code	Pedigree	Protein content (%)	Oil content (%)	Tryptophan content (g / 16g N)	Grain yield /plot (kg)
P_1	BHOML 32-12-6-1-1-⊗#-⊗-⊗	9.59	6.20	0.60	2.14
P_2	BQPML 29-23-5-1-1-⊗-⊗-⊗-⊗	11.93	7.88	0.88	1.39
P_3	BQPML 106-4-2-1-1-⊗-#-⊗-⊗	8.73	5.87	0.61	2.34
P_4	BHOML 45-6-4-1-1-1--⊗-⊗–⊗	11.97	8.06	0.94	1.34
P_5	BQPML 38-3-2-1-1-1-⊗-⊗-⊗	9.84	6.51	0.71	2.12
P_6	BQPML 66-12-5-1-1-1-⊗-⊗-⊗	11.25	7.28	0.80	1.59
P_7	BHOML 131-20-6-1-1-⊗-#-⊗-⊗	11.59	7.58	0.85	1.51
P_8	BHOML 39-4-2-1-1-⊗-#-⊗-⊗	11.00	6.83	0.77	1.64
P_9	BHOML 68-5-2-2-1-1-⊗-⊗-⊗	11.29	7.42	0.80	1.56
P_{10}	BQPML 42-6-3-1-⊗-⊗-#-⊗–⊗	8.93	6.07	0.61	2.16
Entry code	Pedigree	Protein content (%)	Oil content (%)	Tryptophan content (g / 16g N)	Grain yield /plot (kg)
1	P1 x P5	11.03	7.36	0.74	4.34
2	P1 x P8	10.38	6.92	0.66	4.72
3	P1 x P10	10.98	7.53	0.75	4.31
4	P2 x P6	12.05	8.13	0.84	4.17
5	P3 x P5	11.67	7.64	0.81	4.36
6	P3 x P6	10.63	7.11	0.70	4.64
7	P3 x P8	10.80	7.18	0.71	4.67
8	P3 x P9	10.49	7.00	0.68	4.69
9	P3 x P10	11.49	7.58	0.77	4.40
10	P4 x P7	12.03	8.07	0.91	4.19
11	P5 x P10	11.71	7.76	0.81	4.43

best hybrids (except P_4 x P_7) were the combinations of either both the parents as good combiners or one of the parents as good combiner for either grain yield or quality parameters. Among these eleven best specific combiners for grain yield, five crosses namely, P_4 x P_7, P_5 x P_{10}, P_2 x P_6, P_3 x P_5, P_3 x P_9 and P_1 x P_5 were good specific combiners for protein, oil and tryptophan content along with yield (Table 4).

(ii) Stability analysis

Pooled stability analysis of variance revealed the presence of genetic variability among the genotypes for the four characters studied indicating differential response of genotype in different environments and exhibited their indifferent nature of genetic system in controlling the stability performance. Environment linear was also significant for the four characters studied. Significant effect of environment was also reported by other researchers [15-18]. G x E (linear) was found to be significant for all the characters studied except for oil content. It indicates that prediction of the most of the genotypes will be feasible for grain yield, protein content and tryptophan content across locations. Where as for oil content only non linear component alone accounted

Table 3. Estimates of general combining ability effects of ten parents in four environments studied

Parent	Protein content (%)				Oil content (%)				Tryptophan content (g /16g N)				Grain yield /plot (Kg)			
	Kharif 2003		*Kharif* 2004		*Kharif* 2003		*Kharif* 2004		*Kharif* 2003		*Kharif* 2004		*Kharif* 2003		*Kharif* 2004	
	Hyd	Alld	Hyd	Alld	Hyd	Alld	Hyd	Alld	Hyd	Alld	Hyd	Alld	Hyd	Alld	Hyd	Alld
P_1	–0.52**	–0.60**	–0.52**	–0.60**	–0.44**	–0.44**	–0.44**	–0.44**	–0.07**	–0.07**	–0.07**	-0.10**	0.42**	0.45**	0.43**	0.45**
P_2	0.21**	0.24**	0.22**	0.24**	0.13**	0.14*	0.14**	0.14*	0.01**	0.01*	0.01**	0.02**	–0.15**	–0.16**	–0.16**	–0.17**
P_3	–0.44**	–0.41**	–0.43**	–0.42**	–0.22**	–0.22**	–0.22**	–0.22**	–0.05**	–0.05**	–0.05**	-0.04**	0.51**	0.55**	0.52**	0.56**
P_4	0.29**	0.30**	0.29**	0.30**	0.21**	0.21**	0.21**	0.21**	0.06**	0.06**	0.06**	0.05**	–0.36**	–0.38**	–0.36**	–0.39**
P_5	0.02	0.03	0.01	0.03	0.06	0.06	0.06	0.06	0.00	0.00	0.00	0.00	–0.01	0.01*	0.00	0.02**
P_6	0.18**	0.19*	0.18*	0.19*	0.12**	0.11	0.11*	0.11	0.02**	0.02**	0.02**	0.01	0.04**	0.02**	0.03**	0.02**
P_7	0.39**	0.42**	0.39**	0.42**	0.28**	0.28**	0.28**	0.28**	0.04**	0.04**	0.04**	0.04**	–0.43**	–0.44**	–0.44**	–0.44**
P_8	–0.05	–0.04	–0.06	–0.03	–0.12**	–0.11	–0.11*	–0.11	–0.01**	–0.01	–0.01*	0.01	0.06**	0.05**	0.06**	0.04**
P_9	0.11	0.12	0.11	0.12	0.06	0.06	0.06	0.06	0.01**	0.01*	0.01**	0.01	–0.22**	–0.23**	–0.23**	–0.23**
P_{10}	–0.19**	–0.26**	–0.19*	–0.26**	–0.09*	–0.09	–0.09	–0.09	–0.03**	–0.03**	–0.03**	-0.01	0.14**	0.13**	0.14**	0.13**
SE (gi)	0.07	0.10	0.08	0.09	0.28	0.07	0.05	0.07	6.71	0.01	0.00	0.01	0.04	0.01	0.01	0.01
SE (gi-gj)	0.10	0.14	0.12	0.13	0.42	0.10	0.08	0.11	10.00	0.01	0.01	0.02	0.06	0.01	0.01	0.01

Note: Hyd: Hyderabad, Alld: Allahabad; *Significant at 5 per cent level, **Significant at 1 per cent level

for G x E interaction implying that the performance of the genotypes is unpredictable in nature. Pooled stability analysis of variance was presented in Table-5. Kumar *et al.* [19] reported similar type of results in maize crop.

The estimates of stability parameters of parents and hybrids are presented in Table 6 and Table 7, respectively. Among the 45 hybrids studied, the hybrid with regression coefficient (bi) near to unity and non significant deviation from regression (S^2 di) with high means were considered as having average stability. For the most complex and important character grain yield, parents P_3, P_1, P_{10} and P_5 showed high levels of *per se* and stability indicated by non-significant non-linear (S^2 di) estimates. But the linear estimate of G x E interaction, which gives the idea of responsive capacity of a particular genotype, was found to be significant for all the ten parents in respect of grain yield. It is also true for the top ten hybrids namely, P_1 x P_5, P_1 x P_8, P_1 x P_{10}, P_2 x P_6, P_3 x P_6, P_3 x P_8, P_3 x P_9, P_3 x P_{10}, P_4 x P_7 and P_5 x P_{10}. Eberhart and Russel [7] characterized an ideal genotype to be stable, should possess unit regression, lowest deviation from the regression and higher mean to have practical value. Accordingly, above said hybrids were found to be stable for grain yield across the locations having near to unity or unit regression and non-significant deviation from regression along with higher mean values (more than 4.00 kg/plot). Among these ten hybrids P_1 x P_8, P_3 x P_6, P_3 x P_8 and P_3 x P_9 are highest grain yielding hybrids (more than 4.60 kg/plot). Hence, these hybrids can be better utilized for deriving the inbred lines with good grain yield from segregating generations. In respect of three quality characters *viz.,* protein, oil and tryptophan content, the three parents P_4, P_2 and P_7 and the crosses P_4 x P_7, P_2 x P_6 and P_5 x P_{10} (more than 0.80 g/16 g N tryptophan content) exhibited stable performance and higher mean values for all these three characters along with higher mean values (more than 4.00 kg/plot) and stable performance for grain yield.

In brief, from the present investigation it could be inferred that the parents P_3 and P_1were adjudged as best parents followed by P_{10} for grain yield, while parents P_4, P_7 and P_2 for

Table 4. Estimates of specific combining ability effects of top eleven hybrids (Specific combiners) for grain yield in four environments

Best hybrids	Protein content (%)				Oil content (%)			
	Kharif 2003		*Kharif* 2004		*Kharif* 2003		*Kharif* 2004	
	Hyderabad	Allahabad	Hyderabad	Allahabad	Hyderabad	Allahabad	Hyderabad	Allahabad
P1 x P5	0.43	0.5	0.42	0.5	0.57**	0.56**	0.56**	0.56*
P1 x P8	-0.15	-0.08	-0.15	-0.08	0.31*	0.31	0.31	0.31
P1 x P10	1.09**	0.24	1.08**	0.24	0.89**	0.88**	0.88**	0.88**
P2 x P6	0.55*	0.52	0.54*	0.52	0.70**	0.71**	0.71**	0.71**
P3 x P5	0.98**	0.96**	0.98**	0.96**	0.64**	0.63**	0.63**	0.63**
P3 x P6	-0.22	-0.24	-0.23	-0.24	0.03	0.04	0.04	0.04
P3 x P8	0.19	0.16	0.18	0.16	0.35*	0.35	0.35*	0.35
P3 x P9	-0.29	-0.31	-0.29	-0.31	-0.01	0.00	0.00	0.00
P3 x P10	1.01**	1.07**	1.00**	1.07**	0.73**	0.72**	0.72**	0.72**
P4 x P7	0.25	0.22	0.24	0.22	0.42**	0.42	0.42*	0.42
P5 x P10	0.77**	0.85**	0.78**	0.85**	0.63**	0.63**	0.63**	0.63**
SE (S_{ij})	0.23	0.32	0.28	0.29	0.15	0.23	0.18	0.24
SE (S_{ij} -S_{ik})	0.34	0.47	0.41	0.42	0.21	0.34	0.27	0.36

Best hybrids	Tryptophan content (g / 16g N)				Grain yield / plot (Kg)			
	Kharif 2003		*Kharif* 2004		*Kharif* 2003		*Kharif* 2004	
	Hyderabad	Allahabad	Hyderabad	Allahabad	Hyderabad	Allahabad	Hyderabad	Allahabad
P1 x P5	0.05**	0.05*	0.05**	0.05	0.90**	0.96**	0.96**	0.97**
P1 x P8	-0.03**	-0.03	-0.03*	0.00	1.21**	1.30**	1.28**	1.32**
P1 x P10	0.09**	0.09**	0.09**	0.09	0.73**	0.79**	0.79**	0.82**
P2 x P6	0.06**	0.06**	0.06**	0.01	1.26**	1.39**	1.34**	1.40**
P3 x P5	0.10**	0.10**	0.10**	0.06	0.86**	0.90**	0.79**	0.90**
P3 x P6	-0.04**	-0.04	-0.04**	0.00	1.06**	1.15**	1.13**	1.15**
P3 x P8	0.00	0.00	0.00	-0.01	1.06**	1.14**	1.13**	1.18**
P3 x P9	-0.04**	-0.04*	-0.04**	-0.06	1.37**	1.45**	1.45**	1.45**
P3 x P10	0.10**	0.10**	0.10**	0.05	0.72**	0.79**	0.78**	0.81**
P4 x P7	0.06**	0.06**	0.06**	0.05	1.96**	2.08**	2.04**	2.11**
P5 x P10	0.08**	0.08**	0.08**	0.03	1.28**	1.37**	1.34**	1.37**
SE (S_{ij})	0.01	0.02	0.01	0.05	0.05	0.02	0.02	0.02
SE (S_{ij} -S_{ik})	0.02	0.03	0.02	0.07	0.07	0.03	0.03	0.03

*Significant at 5 per cent level, **Significant at 1 per cent level

protein, oil and tryptophan content. Further, out of 45 single crosses studied, the three cross combinations *viz.*, P_4 x P_7, P_2 x P_6 and P_5 x P_{10} were found as good specific combiners and most stable for high grain yield along with high *per se* values for protein, oil and tryptophan contents. Hence, it is suggested that, these three hybrids (*viz.*, P_4 x P_7, P_2 x P_6 and P_5 x P_{10}) can be better exploited as QPM hybrids for commercialization

Table 5. Pooled analysis of variance of 55 genotypes over two locations (Hyderabad and Allahabad) and in two seasons (*kharif* 2003 and *kharif* 2004)

Source	d.f.	Protein content (%)	Oil content (%)	Tryptophan content (g /16 g N)	Grain yield/ plot (kg)
Genotypes	54	2.3244**	1.4172**	0.0278**	4.0624**
Environment + (G x E)	165	0.0093**	0.0178**	0.0010**	0.0065**
Environment (Linear)	1	0.4706**	2.9189**	0.0908**	0.5891**
G x E (Linear)	54	0.0183**	0.0001	0.0007**	0.0071**
Pooled deviation	110	0.0007	0.0001	0.0003	0.0009
Pooled Error	440	0.0838	0.0438	0.0008	0.0010
SE (b) ±		0.2783	3.4317	0.4568	0.2925

**Significant at 1 per cent level

Table 6. Estimates of stability parameters of 10 parents

S.No.	Parents	Protein content			Oil content			Tryptophan content			Grain yield		
		Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
1	P1	9.59	0.82	-0.08	6.20	0.99	-0.04	0.60	4.00**	0.01**	2.14	1.79**	0.00
2	P2	11.93	0.80	-0.08	7.88	0.99	-0.04	0.88	1.61	0.00	1.39	1.79**	0.00
3	P3	8.73	0.81	-0.08	5.87	0.99	-0.04	0.61	0.13	0.00	2.34	1.79**	0.00
4	P4	11.97	0.82	-0.08	8.06	0.99	-0.04	0.94	1.86	0.00	1.34	1.79**	0.00
5	P5	9.84	0.82	-0.08	6.51	0.99	-0.04	0.71	-0.13*	0.00**	2.12	1.79**	0.00
6	P6	11.25	0.82	-0.08	7.28	0.99	-0.04	0.80	0.84	0.00	1.59	1.79**	0.00
7	P7	11.59	0.82	-0.08	7.58	0.99	-0.04	0.85	1.30	0.00	1.51	1.74*	0.00**
8	P8	11.00	0.82	-0.08	6.83	0.99	-0.04	0.77	0.94	0.00	1.64	1.79**	0.00
9	P9	11.29	0.82	-0.08	7.42	0.99	-0.04	0.80	2.07*	0.00**	1.56	1.67*	0.00**
10	P10	8.93	0.81	-0.08	6.07	0.99	-0.04	0.61	0.69	0.00	2.16	1.91**	0.00
Mean of bi			0.9631			0.9991			0.9998			1.0002	
SE of bi			0.2783			0.0343			0.4567			0.2925	

*Significant at 5 per cent level, **Significant at 1 per cent level

Table 7. Estimates of stability parameters of top ten single crosses out of 45 crosses studied

S.No.	Parents	Protein content			Oil content			Tryptophan content			Grain yield		
		Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
1.	P1 x P5	11.03	0.82	-0.08	7.36	0.99	-0.04	0.74	1.25	0.00	4.34	1.86**	0.00
2.	P1 x P8	10.38	0.82	-0.08	6.92	0.99	-0.04	0.66	0.74	0.00	4.72	1.79**	0.00
3.	P1 x P10	10.98	11.05**	-0.06	7.53	0.99	-0.04	0.75	1.30	0.00	4.31	1.74*	0.00
4.	P2 x P6	12.05	0.82	-0.08	8.13	0.99	-0.04	0.84	1.81	0.00	4.17	1.79**	0.00
5.	P3 x P6	10.63	0.82	-0.08	7.11	0.99	-0.04	0.70	0.33	0.00	4.64	1.79**	0.00
6.	P3 x P8	10.80	0.82	-0.08	7.18	0.99	-0.04	0.71	0.74	0.00	4.67	1.98**	0.00
7.	P3 x P9	10.49	0.82	-0.08	7.00	0.99	-0.04	0.68	1.25	0.00	4.69	1.79**	0.00
8.	P3 x P10	11.49	0.82	-0.08	7.58	0.99	-0.04	0.77	1.45	0.00	4.40	1.92**	0.00
9.	P4 x P7	12.03	0.82	-0.08	8.07	0.99	-0.04	0.91	1.40	0.00	4.19	1.86**	0.00
10.	P5 x P10	11.71	0.82	-0.08	7.76	0.99	-0.04	0.81	1.50	0.00	4.43	1.77**	0.00

*Significant at 5 per cent level, **Significant at 1 per cent level across the wide environments through heterosis breeding and also exploited for the derivation of QPM inbred lines in segregating generations.

Acknowledgements

The financial support from Indian Council of Agricultural Research (ICAR) as this research study was conducted in part of NATP-QPM Project is greatly acknowledged. The authors also thank Head of ARS, Amberpet, Hyderabad for providing facilities.

References

1. **Bjarnason M. and Vasal S. K.** 1992. Breeding of quality protein maize (QPM). Plant Breeding Review, **9**: 181-216.
2. **Woodworth C. M., Lang E. R. and Jugenheimer R. W.** 1952. Sixty generations of selections for protein and oil in corn. Agronomy Journal, **44**: 60-65.
3. **Pal A. K. and Prodhan H. S.** 1994. Combining ability analysis of grain yield and oil content along with some other attributes in maize (*Zea mays* L.). Indian J. Genet., **54**: 376-380.
4. **Finley K. W. and Wilkinson G. N.** 1963. The analysis of adaptation of plant breeding programme. Australian Journal of Agricultural Research, **14**: 742-752.
5. **Lin G. Q.** 1992. Study on yield stability in new rice varieties in a regional test in North China. Journal of Genetics and Plant Breeding, **18**: 579-584.
6. **Griffing B.** 1956. A generalized treatment of the use of diallel crosses in quantitative inheritance. Heredity, **10**: 31-50.
7. **Eberhart S. A. and Russell W. A.** 1966. Stability parameters for comparing varieties. Crop Science, **6**: 36-40.
8. **Joshi V. N., Dubey R. B. and Marker S.** 2002. Combining ability for polygenic traits in early maturing hybrids of maize. Indian J. Genet., **62**: 312-315.
9. **Gautam A. S.** 2003. Combining ability studies for grain yield and other agronomic characters in inbred lines of maize (*Zea mays* L.). Crop Research Hisar, **26**: 482-485.
10. **Bhatnagar S., Betran F. J. and Rooney W.** 2004. Combining abilities of Quality Protein Maize inbreds. Crop Science, **44**: 1997-2005.
11. **Prasad R., Singh S. and Paroda R. S.** 1988. Combining ability analysis in a maize diallel. Indian Journal of Genetics and Plant Breeding, **48**: 19-23.
12. **Venkatesh S., Singh N. N. and Gupta N. P.** 2001. Use of inbred testers for evaluating combining ability in modified single cross hybrids of maize. Indian J. Genet., **61**: 309-313.
13. **Venugopal B., Chandramohan Y., Rao N. V. and Reddy V. S.** 2002. Combining ability analysis for quality and grain yield in maize (*Zea mays* L.). National Journal of Plant Improvement, **4**: 50-55.
14. **Suresh J.** 2004. Genetic Analysis of protein and grain yield parameters in selected maize (*Zea mays* L.) genotypes. Ph.D. Thesis submitted to Acharya N. G. Ranga Agricultural University, Rajendranagar, Hyderabad.
15. **Gentinetta E., Mnusardi C., Bertolini M., Snidaro M., Bressan M., Lorenzoni C. and Maggiore T.** 1988. Environmental stability and adaptability for agronomic and qualitative characters of opaque-2 maize hybrids Rivista-di-Agronomia, **22**: 75-80.
16. **Gautam A. S., Bhandari J. C. and Mittal R. K.** 1998. Phenotypic stability for grain yield in maize. Annals of Biology, **14**: 63-65.
17. **Dodiya N. S. and Joshi V. N.** 2003. Genotype x environment interaction and stability analysis for yield and maturity in maize (*Zea mays* L.). Crop-Research-Hisar, **26**: 110-113.
18. **Narasimha Reddy.** 2003. Gentic analysis of yield and its components in selected tropical and sub tropical maize inbreds. Ph.D. Thesis submitted to Acharya N.G. Ranga Agricultural University, Hyderabad.
19. **Kumar P., Gupta S. C. and Nagda A. K.** 1997. Genetics of oil content in maize (*Zea mays* L.). Crop Research, **13**: 333-338.